



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/654,281

Source: 1642 **BEST AVAILABLE COPY**

Date Processed by STIC: 3/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SERIAL NUMBER: 09/654,281

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) 1 contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/654,281

DATE: 03/16/2001
TIME: 15:13:59

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

Does Not Comply
Corrected Diskette Needed

ppr 1-2.5

3 <110> APPLICANT: Sedivy, John
4 Kolch, Walter
5 Yeung, Kam Chi
7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation
8 of Cell Proliferation and Growth
10 <130> FILE REFERENCE: 3564/1010
12 <140> CURRENT APPLICATION NUMBER: 09/654,281
13 <141> CURRENT FILING DATE: 2000-09-01
15 <150> PRIOR APPLICATION NUMBER: 60/151,992
16 <151> PRIOR FILING DATE: 1999-09-01
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 42
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial/Unknown
27 <220> FEATURE:
28 <221> NAME/KEY: UNSURE
29 <222> LOCATION: (3)..(5) Xaa
30 <223> OTHER INFORMATION: X = any amino acid
33 <220> FEATURE:
34 <221> NAME/KEY: UNSURE
35 <222> LOCATION: (9)..(9) delete
36 <223> OTHER INFORMATION: Z = a hydrophobic amino acid residue
39 <220> FEATURE:
40 <221> NAME/KEY: UNSURE
41 <222> LOCATION: (11)..(13) Xaa
42 <223> OTHER INFORMATION: X = any amino acid
45 <220> FEATURE:
46 <221> NAME/KEY: UNSURE
47 <222> LOCATION: (14)..(14) delete
48 <223> OTHER INFORMATION: B = a negatively charged amino acid residue
51 <220> FEATURE:
52 <221> NAME/KEY: UNSURE
53 <222> LOCATION: (15)..(18) Xaa
54 <223> OTHER INFORMATION: X = any amino acid residue
57 <220> FEATURE:
58 <221> NAME/KEY: UNSURE
59 <222> LOCATION: (20)..(21) Xaa
60 <223> OTHER INFORMATION: X = any amino acid residue
63 <220> FEATURE:
64 <221> NAME/KEY: UNSURE
65 <222> LOCATION: (23)..(23) Xaa
66 <223> OTHER INFORMATION: X = between 10 and 50 of any amino acid residue
69 <220> FEATURE:
70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (25)..(28)

) please correct this error
if appears
in subsequent
sequences

invalid - per 1.823 of new Sequence Rules,
the only valid <213> responses are:
Unknown or Artificial Sequence
or scientific name
(genus/species)

(one of the
three)

also,
see item 12
on Error
summary sheet

variable length
not permitted - see
item 6 on Error
summary sheet

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
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Xaa

72 <223> OTHER INFORMATION: (X) = any amino acid residue
 75 <220> FEATURE:
 76 <221> NAME/KEY: UNSURE
 77 <222> LOCATION: (30)...(30) Xaa *see item 6 on Error summary sheet*
 78 <223> OTHER INFORMATION: (X) = between 2 and 4 of any amino acid residue
 81 <220> FEATURE:
 82 <221> NAME/KEY: UNSURE
 83 <222> LOCATION: (32)...(32) Xaa
 84 <223> OTHER INFORMATION: (X) = any amino acid residue
 87 <220> FEATURE:
 88 <221> NAME/KEY: UNSURE
 89 <222> LOCATION: (35)...(35) Xaa
 90 <223> OTHER INFORMATION: (X) = an aromatic amino acid residue
 93 <220> FEATURE:
 94 <221> NAME/KEY: UNSURE
 95 <222> LOCATION: (37)...(37) Xaa
 96 <223> OTHER INFORMATION: (X) = any amino acid residue
 99 <220> FEATURE:
 100 <221> NAME/KEY: UNSURE
 101 <222> LOCATION: (38)...(38) *delete*
 102 <223> OTHER INFORMATION: (Z) = a hydrophobic amino acid residue
 105 <220> FEATURE:
 106 <221> NAME/KEY: UNSURE
 107 <222> LOCATION: (39)...(41) Xaa
 108 <223> OTHER INFORMATION: (X) = any amino acid residue
 111 <400> SEQUENCE: 1
 W--> 113 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
 114 1 5 10 15
 W--> 116 Xaa Xaa Glu Xaa Xaa His Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Gly Xaa
 117 20 25 30
 W--> 119 His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
 120 35 40
 122 <210> SEQ ID NO: 2
 123 <211> LENGTH: 187
 124 <212> TYPE: PRT
 125 <213> ORGANISM: Homo sapiens
 127 <400> SEQUENCE: 2
 129 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
 130 1 5 10 15
 132 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
 133 20 25 30
 135 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
 136 35 40 45
 138 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
 139 50 55 60
 141 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
 142 65 70 75 80
 144 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
 145 85 90 95

RAW SEQUENCE LISTING

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\03162001\I654281.raw

147 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
 148 100 105 110
 150 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
 151 115 120 125
 153 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
 154 130 135 140
 156 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
 157 145 150 155 160
 159 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
 160 165 170 175
 162 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 163 180 185
 165 <210> SEQ ID NO: 3
 166 <211> LENGTH: 187
 167 <212> TYPE: PRT
 168 <213> ORGANISM: Mus musculus
 170 <220> FEATURE:
 171 <221> NAME/KEY: UNSURE
 172 <222> LOCATION: (150)..(150)
 173 <223> OTHER INFORMATION: X = any amino acid residue
 176 <400> SEQUENCE: 3
 178 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
 179 1 5 10 15
 181 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
 182 20 25 30
 184 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
 185 35 40 45
 187 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
 188 50 55 60
 190 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
 191 65 70 75 80
 193 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
 194 85 90 95
 196 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
 197 100 105 110
 199 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
 200 115 120 125
 202 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
 203 130 135 140
 205 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
 206 145 150 155 160
 208 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
 209 165 170 175
 211 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
 212 180 185
 214 <210> SEQ ID NO: 4
 215 <211> LENGTH: 187
 216 <212> TYPE: PRT
 217 <213> ORGANISM: Drosophila

RAW SEQUENCE LISTING

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\03162001\I654281.raw

219 <400> SEQUENCE: 4
 221 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
 222 1 5 10 15
 224 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
 225 20 25 30
 227 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
 228 35 40 45
 230 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
 231 50 55 60
 233 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
 234 65 70 75 80
 236 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
 237 85 90 95
 239 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
 240 100 105 110
 242 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
 243 115 120 125
 245 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
 246 130 135 140
 248 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
 249 145 150 155 160
 251 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
 252 165 170 175
 254 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
 255 180 185
 257 <210> SEQ ID NO: 5
 258 <211> LENGTH: 220
 259 <212> TYPE: PRT
 260 <213> ORGANISM: C. elegans
 262 <400> SEQUENCE: 5
 264 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
 265 1 5 10 15
 267 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
 268 20 25 30
 270 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
 271 35 40 45
 273 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
 274 50 55 60
 276 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
 277 65 70 75 80
 279 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
 280 85 90 95
 282 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
 283 100 105 110
 285 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
 286 115 120 125
 288 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
 289 130 135 140
 291 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln

RAW SEQUENCE LISTING

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292	145	150	155	160												
294	Ser	Gly	Arg	Ile	Glu	Asp	Ala	Glu	His	Gly	Arg	Leu	Thr	Asn	Thr	Ser
295					165				170				175			
297	Gly	Asp	Lys	Arg	Gly	Gly	Trp	Lys	Ala	Ala	Asp	Phe	Val	Ala	Lys	His
298									180		185		190			
300	Lys	Leu	Gly	Ala	Pro	Val	Phe	Gly	Asn	Leu	Phe	Gln	Ala	Glu	Tyr	Asp
301									195		200		205			
303	Asp	Tyr	Val	Pro	Ile	Leu	Asn	Lys	Gln	Leu	Gly	Aia				
304					210				215			220				
306	<210>	SEQ_ID	NO:	6												
307	<211>	LENGTH:	181													
308	<212>	TYPE:	PRT													
309	<213>	ORGANISM:	Antirrhinum-CEN													
311	<400>	SEQUENCE:	6													
313	Met	Ala	Ala	Lys	Val	Ser	Ser	Asp	Pro	Leu	Val	Ile	Gly	Arg	Val	Ile
314	1				5					10			15			
316	Gly	Asp	Val	Val	Asp	His	Phe	Thr	Ser	Thr	Val	Lys	Met	Ser	Val	Ile
317						20			25			30				
319	Tyr	Asn	Ser	Asn	Asn	Ser	Ile	Lys	His	Val	Tyr	Asn	Gly	His	Glu	Leu
320							35		40			45				
322	Phe	Pro	Ser	Ala	Val	Thr	Ser	Thr	Pro	Arg	Val	Glu	Val	His	Gly	Gly
323						50		55			60					
325	Asp	Met	Arg	Ser	Phe	Phe	Thr	Leu	Ile	Met	Thr	Asp	Pro	Asp	Val	Pro
326	65					70			75			80				
328	Gly	Pro	Ser	Asp	Pro	Tyr	Leu	Arg	Glu	His	Leu	His	Trp	Ile	Val	Thr
329						85			90			95				
331	Asp	Ile	Pro	Gly	Thr	Thr	Asp	Ser	Ser	Phe	Gly	Lys	Glu	Val	Val	Ser
332						100		105			110					
334	Tyr	Glu	Met	Pro	Arg	Pro	Asn	Ile	Gly	Ile	His	Arg	Phe	Val	Phe	Leu
335						115		120			125					
337	Leu	Phe	Lys	Gln	Lys	Lys	Arg	Gly	Gln	Ala	Met	Leu	Ser	Pro	Pro	Val
338						130		135			140					
340	Val	Cys	Arg	Asp	Gly	Phe	Asn	Thr	Arg	Lys	Phe	Thr	Gln	Glu	Asn	Glu
341	145						150			155			160			
343	Leu	Gly	Leu	Pro	Val	Ala	Ala	Val	Phe	Phe	Asn	Cys	Gln	Arg	Glu	Thr
344						165			170			175				
346	Ala	Ala	Arg	Arg	Arg											
347					180											
349	<210>	SEQ_ID	NO:	7												
350	<211>	LENGTH:	176													
351	<212>	TYPE:	PRT													
352	<213>	ORGANISM:	Aradopsis-TFL1													
354	<400>	SEQUENCE:	7													
356	Met	Glu	Asn	Met	Gly	Thr	Arg	Val	Ile	Glu	Pro	Leu	Ile	Met	Gly	Arg
357	1				5				10			15				
359	Val	Val	Gly	Asp	Val	Leu	Asp	Phe	Phe	Thr	Pro	Thr	Thr	Lys	Met	Asn
360						20		25			30					
362	Val	Ser	Tyr	Asn	Lys	Lys	Gln	Val	Asn	Gly	His	Glu	Leu	Phe	Pro	Ser
363						35		40			45					

FJ:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/654,281

DATE: 03/16/2001
TIME: 15:14:00

Input Set : A:\PTO.txt
Output Set: N:\CRF3\03162001\I654281.raw

L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10